

### **AMENDMENTS TO SPECIFICATION**

**Replace the paragraph at page 4, lines 13-20, with the following:**

Figures 1A, 1B and 1C present Figure 1 presents an alignment of the amino acid sequences derived from corn clone p0128.cpici34r: fis (SEQ ID NO:18), rice clone r0n.pk099.p14: fis (SEQ ID NO:20), and soybean clone sgs4c.pk003.k23: fis (SEQ ID NO:22) with the *Arabidopsis thaliana* COI1 sequence (NCBI General Identifier No. 3158394; SEQ ID NO:37). Underlined amino acids in SEQ ID NO:37 correspond to the degenerate F-box motif and the 16 imperfect leucine-rich repeats (LRRs) indicated by Xie et al. (1998, *Science* 280:1091-1094). Amino acids conserved among all the species are indicated by an Asterisk (\*) above the alignment. Dashes are used by the program to maximize the alignment.

**Replace the paragraph at page 4, lines 21-28, with the following:**

Figures 2A, 2B and 2C present Figure 2 presents an alignment of the amino acid sequences derived from rice clone rds2c.pk005.b12: fis (SEQ ID NO:30), soybean clone sgc2c.pk001.c22: fis (SEQ ID NO:32), and wheat clone wlmk1.pk0015.h3: fis (SEQ ID NO:36) with the *Zea mays* LLS1 sequence (NCBI General Identifier Nos. 7489721, SEQ ID NO:38). Underlined amino acids in SEQ ID NO:38 correspond to consensus sequence for coordinating the Reiske-type [2Fe-2S] cluster and the mononuclear non-heme binding site (Gray et al. (1997) *Cell* 89:25-31). Amino acids conserved among all sequences are indicated by an Asterisk (\*) above the alignment. Dashes are used by the program to maximize the alignment.

**Replace the paragraph at page 9, lines 3-25, with the following:**

A "substantial portion" of an amino acid or nucleotide sequence comprises an amino acid or a nucleotide sequence that is sufficient to afford putative identification of the protein or gene that the amino acid or nucleotide sequence comprises. Amino acid and nucleotide sequences can be evaluated either manually by one skilled in the art, or by using computer-based sequence comparison and identification tools that employ algorithms such as BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) *J. Mol. Biol.* 215:403-410 ~~Altschul et al. (1993) *J. Mol. Biol.* 215:403-410;~~ ~~see also [www.ncbi.nlm.nih.gov/BLAST/](http://www.ncbi.nlm.nih.gov/BLAST/)~~). In general, a sequence of ten or more contiguous amino acids or thirty or more contiguous nucleotides is necessary in order to putatively identify a polypeptide or nucleic acid sequence as homologous to a known protein or gene. Moreover, with respect to nucleotide sequences, gene-specific oligonucleotide probes comprising 30 or more contiguous nucleotides may

be used in sequence-dependent methods of gene identification (e.g., Southern hybridization) and isolation (e.g., *in situ* hybridization of bacterial colonies or bacteriophage plaques). In addition, short oligonucleotides of 12 or more nucleotides may be used as amplification primers in PCR in order to obtain a particular nucleic acid fragment comprising the primers. Accordingly, a "substantial portion" of a nucleotide sequence comprises a nucleotide sequence that will afford specific identification and/or isolation of a nucleic acid fragment comprising the sequence. The instant specification teaches amino acid and nucleotide sequences encoding polypeptides that comprise one or more particular plant proteins. The skilled artisan, having the benefit of the sequences as reported herein, may now use all or a substantial portion of the disclosed sequences for purposes known to those skilled in this art. Accordingly, the instant invention comprises the complete sequences as reported in the accompanying Sequence Listing, as well as substantial portions of those sequences as defined above.

**Replace the paragraph beginning at page 20, line 25, and continuing through page 21, line 2, with the following:**

cDNA clones encoding disease resistance factors were identified by conducting BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) *J. Mol. Biol.* 215:403-410 ~~Altschul et al. (1993) *J. Mol. Biol.* 215:403-410~~; see also [www.ncbi.nlm.nih.gov/BLAST/](http://www.ncbi.nlm.nih.gov/BLAST/)) searches for similarity to sequences contained in the BLAST "nr" database (comprising all non-redundant GenBank CDS translations, sequences derived from the 3-dimensional structure Brookhaven Protein Data Bank, the last major release of the SWISS-PROT protein sequence database, EMBL, and DDBJ databases). The cDNA sequences obtained in Example 1 were analyzed for similarity to all publicly available DNA sequences contained in the "nr" database using the BLASTN algorithm provided by the National Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the "nr" database using the BLASTX algorithm (Gish and States (1993) *Nat. Genet.* 3:266-272) provided by the NCBI. For convenience, the P-value (probability) of observing a match of a cDNA sequence to a sequence contained in the searched databases merely by chance as calculated by BLAST are reported herein as "pLog" values, which represent the negative of the logarithm of the reported P-value. Accordingly, the greater the pLog value, the greater the likelihood that the cDNA sequence and the BLAST "hit" represent homologous proteins.

**Replace the paragraph at page 22, lines 4-10, with the following:**

Figures 1A, 1B and 1C present ~~Figure 1~~ presents an alignment of the amino acid sequences set forth in SEQ ID NOs:18, 20, and 22 and the *Arabidopsis thaliana* sequence (NCBI General Identifier No. 3158394; SEQ ID NO:37). Underlined amino acids in SEQ ID NO:37 correspond to the degenerate F-box motif and the 16 imperfect leucine-rich repeats (LRRs) indicated by Xie et al. (1998, *Science* 280:1091-1094). The data in Table 5 presents a calculation of the percent identity of the amino acid sequences set forth in SEQ ID NOs:2, 4, 6, 8, 16, 18, 20, 22, 24, 26, and 28 and the *Arabidopsis thaliana* COI1 protein sequence (SEQ ID NO:37).

**Replace the paragraph at page 24, lines 7-13, with the following:**

Figures 2A, 2B and 2C present ~~Figure 2~~ presents an alignment of the amino acid sequences set forth in SEQ ID NOs:30, 32, and 36 and the *Zea mays* sequence (NCBI General Identifier Nos. 7489721, SEQ ID NO:38). Underlined amino acids in SEQ ID NO:38 correspond to the consensus sequence for coordinating the Reiske-type [2Fe-2S] cluster and the mononuclear non-heme binding site (Gray et al. (1997) *Cell* 89:25-31) The data in Table 8 presents a calculation of the percent identity of the amino acid sequences set forth in SEQ ID NOs:10, 12, 14, 30, 32, and 36 and the *Zea mays* sequence (SEQ ID NO:38).